

Corrigendum

Portal protein diversity and phage ecology

Matthew B. Sullivan,¹ Maureen L. Coleman,¹ Vanessa Quinlivan,² Jessica E. Rosenkrantz,² Alicia S. DeFrancesco,² G. Tan,² Ross Fu,¹ Jessica A. Lee,² John B. Waterbury,³ Joseph P. Bielawski⁴ and Sallie W. Chisholm^{1,2*}

Departments of ¹Civil and Environmental Engineering and ²Biology, Massachusetts Institute of Technology, Cambridge, MA 02139, USA.

³Department of Biology, Woods Hole Oceanographic Institution, Woods Hole, MA 02543, USA.

⁴Department of Biology, Dalhousie University, Nova Scotia, Canada.

Recent whole genome cyanophage sequencing (Sullivan et al 2010) has revealed that the sequences of some genes do not match those published previously as single gene sequences derived from DNA fragments PCR-amplified from phage isolates. Specifically, the g20 gene sequences for S-SSM7 (gene GI:189397276, protein GI:189397277) and Syn33 (gene GI:189397306, protein GI:189397307) in Sullivan et al. 2008 were incorrect. The GenBank entries have now been corrected. The revised sequences do not alter g20 tree topology or the conclusions of Sullivan et al (2008).

The source of error for these gene sequences is not certain, but could have its origin in either a clerical error, PCR contamination, and/or mixed phage stocks. On this latter point, it has recently come to light that triplicate plaque purifications do not always result in pure stocks for these cyanophages, possibly due to the fluid consistency of the agarose plates (0.28% agarose) required for growth of the host. More reliable purification procedures have subsequently been developed. However, as mixed phage stock preparations could influence host range, we recommend that published host range data (Sullivan et al 2003) be verified before their use in further research.

References

- Sullivan, M.B., Coleman, M.L., Quinlivan, V., Rosenkrantz, J.R., DeFrancesco, A.S., Tan, G.P. et al. (2008) Portal protein diversity and phage ecology. *Environmental Microbiology* **10**: 2810-2823.
- Sullivan, M.B., Huang, K.H., Ignacio-Espinoza, J.C., Berlin, A., Kelly, L., Weigele, P.R. et al. (2010) Genomic analysis of oceanic cyanobacterial myoviruses compared to T4-like myoviruses from diverse hosts and environments. *Environ Microbiol* **12**: 3035-3056.

*For correspondence. E-mail chisholm@mit.edu; Tel. (+1) 617 253 1771; Fax (+1) 617 324 0336.